

ABSTRACT OF THE DISCLOSURE

The present invention relates to a method for identifying unknown molecular interactions within biological networks based on representations of molecules as sets of conserved features. Such molecules include but are not limited to proteins and nucleic acid molecules which can be represented as collections of conserved features, such as domains and motifs in proteins. The method of the invention comprises computing the attraction probabilities between molecules followed by calculation of the probability of a biological network. The method of the invention can be applied across species, where interaction data from one, or several species, can be used to infer molecular interactions between molecules acting within or between organisms. The method of the present invention may be used to identify molecular interactions which can serve as drug screening targets.